SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: Scott, Matthew P.
                Goodrich, Lisa V.
                Johnson, Ronald L.

    (ii) TITLE OF INVENTION: Mammalian Patched Gene and Its Use

   (iii) NUMBER OF SEQUENCES: 20

    (iv) CORRESPONDENCE ADDRESS:
        (A) ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
        (B) STREET: 4 Embarcadero Center, Suite 3400
        (C) CITY: San Francisco
        (D) STATE: California
        (E) COUNTRY: USA
        (F) ZIP: 94111-4187

    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

    (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER:
        (B) FILING DATE:
        (C) CLASSIFICATION:

  (viii) ATTORNEY/AGENT INFORMATION:
        (A) NAME: Rowland, Bertram I
        (B) REGISTRATION NUMBER: 20,015
        (C) REFERENCE/DOCKET NUMBER: A60190/BIR STAN171

    (ix) TELECOMMUNICATION INFORMATION:
        (A) TELEPHONE: (415) 781-1989
        (B) TELEFAX: (415) 398-3249
        (C) TELEX: 910277299

(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 680 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
AACCTATGGC ACCCCCCCCA ACCTTTCCTA ACAAAACCCC TTTATACCCC CTTAAATTTT      60

CCACCCAAAC CCTGAACAGA AACCTTTTTA ACCCCCCCCA CCCGGAATTC CATCCCCCCC     120
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AAATTACAAC TCCAGCCAAA ATTAAAATTG GTCCTAACCT AACCATGTTG TTACGGTTTC   180

CCCCCCCAAA TACATGCACT GGCCCGAACA CTTGATCGTT GCCGTTCCAA TAAGAATAAA   240

TCTGGTCATA TTAAACAAGC CAAAGCTTTA CAAACTGTTG TACAATTAAT GGGCGAACAC   300

GAACTGTTCG AATTCTGGTC TGGACATTAC AAAGTGCACC ACATCGGATG GAACCAGGAG   360

AAGGCCACAA CCGTACTGAA CGCCTGGCAG AAGAAGTTCG CACAGGTTGG TGGTTGGCGC   420

AAGGAGTAGA GTGAATGGTG GTAATTTTTG GTTGTTCCAG GAGGTGGATC GTCTGACGAA   480

GAGCAAGAAG TCGTCGAATT ACATCTTCGT GACGTTCTCC ACCGCCAATT TGAACAAGAT   540

GTTGAAGGAG GCGTCGAAAC GGACGTGGTG AAGCTGGGGG TGGTGCTGGG GGTGGCGGCG   600

GTGTACGGGT GGGTGGCCCA GTCGGGGCTG GCTGCCTTGG GAGTGCTGGT CTTGCGGCTC   660

ATTCGCCCTA TAGTAGCGTA   680

(2) INFORMATION FOR SEQ ID NO:2:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 107 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: protein

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

        Xaa Pro Pro Pro Asn Tyr Asn Ser Xaa Pro Lys Xaa Xaa Xaa Leu Val
        1   5   10   15

        Leu Thr Pro Xaa Val Val Thr Val Ser Pro Pro Lys Tyr Met His Trp
                        20   25   30

        Pro Glu His Leu Ile Val Ala Val Pro Ile Arg Ile Asn Leu Val Ile
                    35   40   45

        Leu Asn Lys Pro Lys Ala Leu Gln Thr Val Val Gln Leu Met Gly Glu
            50   55   60

        His Glu Leu Phe Glu Phe Trp Ser Gly His Tyr Lys Val His His Ile
        65   70   75   80

        Gly Trp Asn Gln Glu Lys Ala Thr Thr Val Leu Asn Ala Trp Gln Lys
                        85   90   95

        Lys Phe Ala Gln Val Gly Gly Trp Arg Lys Glu
                        100   105

(2) INFORMATION FOR SEQ ID NO:3:

        (i) SEQUENCE CHARACTERISTICS:

2

(A) LENGTH: 4448 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: cDNA

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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GGCCAGTGTC GACACGCTGT TAAGGTGTTA CGAAACTATC GAAACTCTGT ACCGTTCCGT      60

GTTACATTCG GTCAGTGATA AACAGAAGTG AATAATTCGG GTGTACAAGT GTGTGGTTAT     120

GTGGCGGCGA GTGATATGAC AGCGTGCGCC GCCAGACGGA TTCCAGCCGT CTTCATGAGG     180

ATATCGGTGA CAAGCCTGGC CCCGAGATCA TGGTGGCTCC CGATTCCGAG GCTCCTTCGA     240

ATCCTCGGAT AACGGCTGCA CACGAGAGCC CCTGCGCCAC CGAGGCGCGC CACAGTGCTG     300

ATCTTTACAT ACGTACCAGT TGGGTGGACG CCGCACTAGC TCTCTCTGAA CTCGAAAAGG     360

GTAACATCGA AGGAGGAAGA ACCTCTCTGT GGATACGAGC GTGGCTACAA GAACAGCTCT     420

TTATTTTGGG CTGCTTTCTT CAAGGCGACG CGGGGAAAGT CCTCTTCGTT GCCATCCTCG     480

TTCTGTCGAC GTTCTGCGTC GGTCTCAAGT CAGCACAAAT ACATACAAGG GTCGACCAAC     540

TCTGGGTTCA AGAGGGTGGT AGATTAGAAG CCGAGTTGAA ATATACAGCG CAAGCTTTGG     600

GCGAGGCGGA CTCCTCGACG CACCAGCTTG TCATACAAAC TGCCAAAGAT CCAGACGTCT     660

CCCTGCTACA TCCAGGCGCG TTGCTTGAAC ACCTTAAGGT GGTGCACGCA GCGACTCGGG     720

TGACAGTTCA CATGTACGAC ATTGAGTGGC GCCTCAAAGA CCTGTGCTAC AGCCCCAGCA     780

TACCGGACTT CGAGGGTTAC CACCACATCG AGTCAATCAT AGACAACGTC ATCCCCTGCG     840

CTATTATCAC CCCCCTTGAT TGCTTCTGGG AAGGCTCCAA GTTGCTTGGT CCCGATTATC     900

CTATATACGT ACCACATCTT AAACACAAAC TACAATGGAC ACATTAAAT CCATTGGAAG      ·960

TTGTAGAAGA AGTGAAAAAA TTAAAGTTCC AATTTCCTCT GAGCACAATA GAGGCGTACA    1020

TGAAGAGAGC CGGCATCACT TCCGCCTACA TGAAAAAGCC GTGCTTAGAC CCCACCGACC    1080

CACATTGTCC AGCCACGGCT CCAAACAAAA AGTCTGGTCA TATTCCAGAT GTAGCGGCGG    1140

AGCTGTCGCA CGGATGTTAT GGTTTCGCGG CAGCTTACAT GCACTGGCCG GAACAGTTAA    1200

TTGTAGGGGG AGCTACAAGG AATTCGACAT CAGCTCTGAG AAAAGCACGC GTTTACAGAC    1260

TGTAGTACAG TTAATGGGCG AGAGAGAAAT GTACGAGTAC TGGGCCGATC ATTATAAAGT    1320

ACATCAAATT GGCTGGAATC AAGAGAAGGC AGCTGCTGTA CTGGATGCCT GGCAGAGAAA    1380

GTTTGCCGCT GAAGTCAGAA AAATTACTAC CTCAGGATCA GTATCATCGG CTTATAGTTT    1440
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3

CTATCCGTTC TCCACCTCGA CACTTAATGA CATACTCGGG AAGTTCTCCG AAGTGTCACT   1500

GAAGAACATT ATATTAGGCT ATATGTTTAT GTTAATTTAT GTTGCCGTTA CTTTAATACA   1560

ATGGCGGGAT CCGATTCGCT CGCAAGCGGG TGTGGGTATC GCCGGAGTTC TACTACTATC   1620

AATCACTGTT GCCGCTGGCT TAGGATTTTG TGCTTTATTA GGCATACCAT TCAACGCTTC   1680

AAGTACGCAA ATAGTACCAT TCCTAGCGCT CGGGTTAGGA GTTCAAGATA TGTTTCTTCT   1740

CACTCACACG TATGTGGAGC AAGCGGGAGA TGTGCCTAGA GAAGAGAGGA CTGGACTTGT   1800

ATTGAAAAAG AGCGGTTTAA GCGTACTTCT GGCGTCTTTG TGCAACGTGA TGGCATTTTT   1860

GGCAGCAGCC CTTCTACCTA TTCCAGCTTT CAGAGTATTT TGCCTACAGG CTGCCATACT   1920

TCTTCTGTTT AACTTGGGGT CAATATTACT GGTTTTTCCT GCTATGATCT CGTTAGACCT   1980

GCGACGGAGG TCAGCCGCGA GGGCCGATCT TTTATGCTGT TTGATGCCTG AGAGTCCATT   2040

ACCGAAGAAG AAAATTCCGG AAAGAGCAAA AACTAGAAAA AACGATAAGA CTCATAGGAT   2100

AGACACCACG AGACAACCTC TAGACCCAGA TGTGTCCGAG AACGTGACCA AAACTTGCTG   2160

CTTAAGCGTC TCGCTCACCA AGTGGGCCAA GAACCAATAC GCGCCGTTCA TCATGCGCCC   2220

CGCTGTTAAG GTTACATCCA TGTTAGCGTT GATTGCTGTT ATTCTGACTA GCGTTTGGGG   2280

AGCGACAAAA GTAAAGGATG GATTGGATTT GACTGATATT GTACCGGAGA ATACAGACGA   2340

ACACGAATTT TTATCTCGTC AGGAAAAATA CTTTGGCTTC TATAATATGT ACGCCGTGAC   2400

GCAAGGCAAC TTTGAATATC CCACCAATCA GAAGTTATTA TATGAGTATC ACGATCAATT   2460

CGTCAGAATA CCTAATATAA TCAAGAATGA TAACGGCGGT CTCACGAAAT TTTGGTTGAG   2520

TTTATTCCGC GACTGGTTAT TGGACTTGCA AGTGGCTTTT GATAAGGAGG TTGCCAGCGG   2580

TTGTATAACA CAAGAGTATT GGTGCAAAAA CGCGAGTGAC GAAGGAATAT TGGCCTATAA   2640

ACTTATGGTG CAGACTGGCC ATGTGGACAA TCCAATCGAT AAGTCTCTGA TTACGGCAGG   2700

TCACAGACTA GTTGACAAAG ACGGTATTAT AAATCCAAAG GCATTTTATA ATTACCTATC   2760

AGCTTGGGCT ACTAACGACG CGTTGGCATA CGGAGCCTCA CAAGGGAACT TGAAACCTCA   2820

GCCCCAAAGA TGGATCCATT CTCCGGAGGA TGTACATTTA GAAATAAAGA AATCGTCGCC   2880

ATTAATTTAC ACACAGTTAC CATTCTACCT TTCCGGTCTC AGCGACACTA TAGCATCAAA   2940

ACGTTGATAA GATCTGTGCG AGATTTATGT CTGAAGTACG AGGCGAAAGG TTTACCGAAC   3000

TTTCCATCGG GTATACCATT CCTTTTCTGG GAACAGTATT TGTATTTAAG GACATCTTTA   3060

CTACTGGCTT TGGCGTGTGC TTTGGCAGCT GTCTTCATTG CGGTTATGGT GCTATTGTTG   3120

AACGCCTGGG CAGCAGTACT GGTGACATTA GCGCTGGCTA CATTAGTACT GCAGCTGTTA   3180

4

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GGTGTATGGC CTTATTGGGC GTGAAGCTAT CTGCAATGCC GGCCGTACTA CTGGTGCTAG     3240

CCATTGGGAG AGGAGTTCAC TTCACTGTGC ATTTATGTTT GGGTTTTGTA ACATCAATCG     3300

GTTGCAAGCG GCGCCGCGCG TCACTAGCTC TAGAATCAGT TCTGGCGCCA GTGGTGCACG     3360

GCGCTCTGGC GGCCGCGCTG GCTGCCTCGA TGCTAGCTGC AAGTGAATGT GGCTTCGTTG     3420

CCAGACTGTT CTTGAGGTTA CTACTGGACA TCGTGTTTCT GGGACTCATC GATGGGTTGC     3480

TGTTCTTCCC TATTGTCCTT TCGATATTGG GACCGGCTGC TGAGGTACGA CCTATAGAGC     3540

ATCCAGAACG CTTATCGACT CCATCGCCAA AATGTTCGCC CATCCACCCT CGCAAATCAA     3600

GTTCCAGCTC AGGCGGTGGT GATAAATCAA GTCGAACCAG TAAATCAGCA CCAAGGCCTT     3660

GCGCACCATC TCTCACGACC ATTACTGAAG AGCCTTCGAG TTGGCACAGT TCCGCCCACT     3720

CCGTACAATC TTCTATGCAG TCGATAGTGG TCCAGCCGGA GGTGGTGGTC GAAACTACCA     3780

CGTATAATGG CAGCGATTCT GCTTCAGGAC GGTCGACGCC TACAAAGTCT TCACACGGTG     3840

GTGCTATCAC AACTACTAAG GTGACCGCCA CGGCAAATAT AAAGGTAGAA GTGGTGACAC     3900

CGAGTGACAG GAAATCGCGA CGTTCCTATC ATTACTATGA TCGTCGAAGG GATCGCGATG     3960

AAGATAGGGA TCGAGACCGT GAAAGGGACA GAGATCGCGA CAGGGATCGG GATAGGGATC     4020

GTGACCGGGA CAGGGATAGG GATAGAGAAC GATCGAGAGA ACGAGACAGG CGAGACCGAT     4080

ATAGAGACGA AAGGGACCAC CGAGCTTCGC CGAGAGAAAA ACGGCAGAGA TTCTGGACAT     4140

GAAAGTGATT CATCACGTCA TTAAGGATGA AGTACATTGC CAACTTGCCA GAAACGCTCG     4200

TACAGTCGCG GTATCTGAAC ATATACCGGT TGCGTTATTG AATAACTTGT AAATGATCTC     4260

TTTGATTCGG CTTAAACATA TTTTAGTTCA CATCCTGCAA CATCTTAATA CGGTTAGGGT     4320

TAATTTTAAG TCCATAATAG TCGTATGTGG TTGGTCCTTG CGTTAAGTGC ATTAGTTTTT     4380

TCCCATCACT GGGTCCGTGG CTTTTAATTT GGTTTAACGG GGGGGGACCT TTTTTTTTTT     4440

TTTTTTTG                                                             4448
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(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1311 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Ala Pro Asp Ser Glu Ala Pro Ser Asn Pro Arg Ile Thr Ala
1   5   10   15

Ala His Glu Ser Pro Cys Ala Thr Glu Ala Arg His Ser Ala Asp Leu
            20   25   30

Tyr Ile Arg Thr Ser Trp Val Asp Ala Ala Leu Ala Leu Ser Glu Leu
        35   40   45

Glu Lys Gly Asn Ile Glu Gly Gly Arg Thr Ser Leu Trp Ile Arg Ala
        50   55   60

Trp Leu Gln Glu Gln Leu Phe Ile Leu Gly Cys Phe Leu Gln Gly Asp
65   70   75   80

Ala Gly Lys Val Leu Phe Val Ala Ile Leu Val Leu Ser Thr Phe Cys
            85   90   95

Val Gly Leu Lys Ser Ala Gln Ile His Thr Arg Val Asp Gln Leu Trp
            100   105   110

Val Gln Glu Gly Gly Arg Leu Glu Ala Glu Leu Lys Tyr Thr Ala Gln
        115   120   125

Ala Leu Gly Glu Ala Asp Ser Ser Thr His Gln Leu Val Ile Gln Thr
    130   135   140

Ala Lys Asp Pro Asp Val Ser Leu Leu His Pro Gly Ala Leu Leu Glu
145   150   155   160

His Leu Lys Val Val His Ala Ala Thr Arg Val Thr Val His Met Tyr
            165   170   175

Asp Ile Glu Trp Arg Leu Lys Asp Leu Cys Tyr Ser Pro Ser Ile Pro
        180   185   190

Asp Phe Glu Gly Tyr His His Ile Glu Ser Ile Ile Asp Asn Val Ile
        195   200   205

Pro Cys Ala Ile Ile Thr Pro Leu Asp Cys Phe Trp Glu Gly Ser Lys
    210   215   220

Leu Leu Gly Pro Asp Tyr Pro Ile Tyr Val Pro His Leu Lys His Lys
225   230   235   240

Leu Gln Trp Thr His Leu Asn Pro Leu Glu Val Val Glu Glu Val Lys
            245   250   255

Lys Leu Lys Phe Gln Phe Pro Leu Ser Thr Ile Glu Ala Tyr Met Lys
        260   265   270

Arg Ala Gly Ile Thr Ser Ala Tyr Met Lys Lys Pro Cys Leu Asp Pro
        275   280   285

Thr Asp Pro His Cys Pro Ala Thr Ala Pro Asn Lys Lys Ser Gly His
    290   295   300

Ile Pro Asp Val Ala Ala Glu Leu Ser His Gly Cys Tyr Gly Phe Ala

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305                     310                     315                     320
Ala Ala Tyr Met His Trp Pro Glu Gln Leu Ile Val Gly Gly Ala Thr
            325                     330                     335

Arg Asn Ser Thr Ser Ala Leu Arg Lys Ala Arg Xaa Leu Gln Thr Val
            340                     345                     350

Val Gln Leu Met Gly Glu Arg Glu Met Tyr Glu Tyr Trp Ala Asp His
            355                     360                     365

Tyr Lys Val His Gln Ile Gly Trp Asn Gln Glu Lys Ala Ala Ala Val
    370                     375                     380

Leu Asp Ala Trp Gln Arg Lys Phe Ala Ala Glu Val Arg Lys Ile Thr
385                     390                     395                     400

Thr Ser Gly Ser Val Ser Ser Ala Tyr Ser Phe Tyr Pro Phe Ser Thr
                405                     410                     415

Ser Thr Leu Asn Asp Ile Leu Gly Lys Phe Ser Glu Val Ser Leu Lys
            420                     425                     430

Asn Ile Ile Leu Gly Tyr Met Phe Met Leu Ile Tyr Val Ala Val Thr
        435                     440                     445

Leu Ile Gln Trp Arg Asp Pro Ile Arg Ser Gln Ala Gly Val Gly Ile
    450                     455                     460

Ala Gly Val Leu Leu Leu Ser Ile Thr Val Ala Ala Gly Leu Gly Phe
465                     470                     475                     480

Cys Ala Leu Leu Gly Ile Pro Phe Asn Ala Ser Ser Thr Gln Ile Val
                485                     490                     495

Pro Phe Leu Ala Leu Gly Leu Gly Val Gln Asp Met Phe Leu Leu Thr
            500                     505                     510

His Thr Tyr Val Glu Gln Ala Gly Asp Val Pro Arg Glu Glu Arg Thr
            515                     520                     525

Gly Leu Val Leu Lys Lys Ser Gly Leu Ser Val Leu Leu Ala Ser Leu
    530                     535                     540

Cys Asn Val Met Ala Phe Leu Ala Ala Ala Leu Leu Pro Ile Pro Ala
545                     550                     555                     560

Phe Arg Val Phe Cys Leu Gln Ala Ala Ile Leu Leu Leu Phe Asn Leu
                565                     570                     575

Gly Ser Ile Leu Leu Val Phe Pro Ala Met Ile Ser Leu Asp Leu Arg
            580                     585                     590

Arg Arg Ser Ala Ala Arg Ala Asp Leu Leu Cys Cys Leu Met Pro Glu
    595                     600                     605

Ser Pro Leu Pro Lys Lys Lys Ile Pro Glu Arg Ala Lys Thr Arg Lys
    610                     615                     620
```

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Asn Asp Lys Thr His Arg Ile Asp Thr Thr Arg Gln Pro Leu Asp Pro
625   630   635   640

Asp Val Ser Glu Asn Val Thr Lys Thr Cys Cys Leu Ser Val Ser Leu
                645   650   655

Thr Lys Trp Ala Lys Asn Gln Tyr Ala Pro Phe Ile Met Arg Pro Ala
            660   665   670

Val Lys Val Thr Ser Met Leu Ala Leu Ile Ala Val Ile Leu Thr Ser
        675   680   685

Val Trp Gly Ala Thr Lys Val Lys Asp Gly Leu Asp Leu Thr Asp Ile
    690   695   700

Val Pro Glu Asn Thr Asp Glu His Glu Phe Leu Ser Arg Gln Glu Lys
705   710   715   720

Tyr Phe Gly Phe Tyr Asn Met Tyr Ala Val Thr Gln Gly Asn Phe Glu
                725   730   735

Tyr Pro Thr Asn Gln Lys Leu Leu Tyr Glu Tyr His Asp Gln Phe Val
            740   745   750

Arg Ile Pro Asn Ile Ile Lys Asn Asp Asn Gly Gly Leu Thr Lys Phe
        755   760   765

Trp Leu Ser Leu Phe Arg Asp Trp Leu Leu Asp Leu Gln Val Ala Phe
    770   775   780

Asp Lys Glu Val Ala Ser Gly Cys Ile Thr Gln Glu Tyr Trp Cys Lys
785   790   795   800

Asn Ala Ser Asp Glu Gly Ile Leu Ala Tyr Lys Leu Met Val Gln Thr
                805   810   815

Gly His Val Asp Asn Pro Ile Asp Lys Ser Leu Ile Thr Ala Gly His
        820   825   830

Arg Leu Val Asp Lys Asp Gly Ile Ile Asn Pro Lys Ala Phe Tyr Asn
        835   840   845

Tyr Leu Ser Ala Trp Ala Thr Asn Asp Ala Leu Ala Tyr Gly Ala Ser
    850   855   860

Gln Gly Asn Leu Lys Pro Gln Pro Gln Arg Trp Ile His Ser Pro Glu
865   870   875   880

Asp Val His Leu Glu Ile Lys Lys Ser Ser Pro Leu Ile Tyr Thr Gln
            885   890   895

Leu Pro Phe Tyr Leu Ser Gly Leu Ser Asp Thr Xaa Ser Ile Lys Thr
            900   905   910

Leu Ile Arg Ser Val Arg Asp Leu Cys Leu Lys Tyr Glu Ala Lys Gly
        915   920   925

Leu Pro Asn Phe Pro Ser Gly Ile Pro Phe Leu Phe Trp Glu Gln Tyr

8

Leu Tyr Leu Arg Thr Ser Leu Leu Leu Ala Leu Ala Cys Ala Leu Ala
945 950 955 960

Ala Val Phe Ile Ala Val Met Val Leu Leu Leu Asn Ala Trp Ala Ala
965 970 975

Val Leu Val Thr Leu Ala Leu Ala Thr Leu Val Leu Gln Leu Leu Gly
980 985 990

Val Met Ala Leu Leu Gly Val Lys Leu Ser Ala Met Pro Ala Val Leu
995 1000 1005

Leu Val Leu Ala Ile Gly Arg Gly Val His Phe Thr Val His Leu Cys
1010 1015 1020

Leu Gly Phe Val Thr Ser Ile Gly Cys Lys Arg Arg Arg Ala Ser Leu
1025 1030 1035 1040

Ala Leu Glu Ser Val Leu Ala Pro Val Val His Gly Ala Leu Ala Ala
1045 1050 1055

Ala Leu Ala Ala Ser Met Leu Ala Ala Ser Glu Cys Gly Phe Val Ala
1060 1065 1070

Arg Leu Phe Leu Arg Leu Leu Leu Asp Ile Val Phe Leu Gly Leu Ile
1075 1080 1085

Asp Gly Leu Leu Phe Phe Pro Ile Val Leu Ser Ile Leu Gly Pro Ala
1090 1095 1100

Ala Glu Val Arg Pro Ile Glu His Pro Glu Arg Leu Ser Thr Pro Ser
1105 1110 1115 1120

Pro Lys Cys Ser Pro Ile His Pro Arg Lys Ser Ser Ser Ser Ser Gly
1125 1130 1135

Gly Gly Asp Lys Ser Ser Arg Thr Ser Lys Ser Ala Pro Arg Pro Cys
1140 1145 1150

Ala Pro Ser Leu Thr Thr Ile Thr Glu Glu Pro Ser Ser Trp His Ser
1155 1160 1165

Ser Ala His Ser Val Gln Ser Ser Met Gln Ser Ile Val Val Gln Pro
1170 1175 1180

Glu Val Val Val Glu Thr Thr Thr Tyr Asn Gly Ser Asp Ser Ala Ser
1185 1190 1195 1200

Gly Arg Ser Thr Pro Thr Lys Ser Ser His Gly Gly Ala Ile Thr Thr
1205 1210 1215

Thr Lys Val Thr Ala Thr Ala Asn Ile Lys Val Glu Val Val Thr Pro
1220 1225 1230

Ser Asp Arg Lys Ser Arg Arg Ser Tyr His Tyr Tyr Asp Arg Arg Arg
1235 1240 1245

9

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Asp Arg Asp Glu Asp Arg Asp Arg Asp Arg Glu Arg Asp Arg Asp Arg
    1250              1255              1260

Asp Arg Asp Arg Asp Arg Asp Arg Asp Arg Asp Arg Asp Arg Asp Arg
    1265              1270              1275              1280

Glu Arg Ser Arg Glu Arg Asp Arg Arg Asp Arg Tyr Arg Asp Glu Arg
              1285              1290              1295

Asp His Arg Ala Ser Pro Arg Glu Lys Arg Gln Arg Phe Trp Thr
        1300              1305              1310
```

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4434 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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CGAAACAAGA GAGCGAGTGA GAGTAGGGAG AGCGTCTGTG TTGTGTGTTG AGTGTCGCCC      60

ACGCACACAG GCGCAAAACA GTGCACACAG ACGCCCGCTG GGCAAGAGAG AGTGAGAGAG     120

AGAAACAGCG GCGCGCGCTC GCCTAATGAA GTTGTTGGCC TGGCTGGCGT GCCGCATCCA     180

CGAGATACAG ATACATCTCT CATGGACCGC GACAGCCTCC CACGCGTTCC GGACACACAC     240

GGCGATGTGG TCGATGAGAA ATTATTCTCG GATCTTTACA TACGCACCAG CTGGGTGGAC     300

GCCCAAGTGG CGCTCGATCA GATAGATAAG GGCAAAGCGC GTGGCAGCCG CACGGCGATC     360

TATCTGCGAT CAGTATTCCA GTCCCACCTC GAAACCCTCG GCAGCTCCGT GCAAAAGCAC     420

GCGGGCAAGG TGCTATTCGT GGCTATCCTG GTGCTGAGCA CCTTCTGCGT CGGCCTGAAG     480

AGCGCCCAGA TCCACTCCAA GGTGCACCAG CTGTGGATCC AGGAGGGCGG CCGGCTGGAG     540

GCGGAACTGG CCTACACACA GAAGACGATC GGCGAGGACG AGTCGGCCAC GCATCAGCTG     600

CTCATTCAGA CGACCCACGA CCCGAACGCC TCCGTCCTGC ATCCGCAGGC GCTGCTTGCC     660

CACCTGGAGG TCCTGGTCAA GGCCACCGCC GTCAAGGTGC ACCTCTACGA CACCGAATGG     720

GGGCTGCGCG ACATGTGCAA CATGCCGAGC ACGCCCTCCT TCGAGGGCAT CTACTACATC     780

GAGCAGATCC TGCGCCACCT CATTCCGTGC TCGATCATCA CGCCGCTGGA CTGTTTCTGG     840

GAGGGAAGCC AGCTGTTGGG TCCGGAATCA GCGGTCGTTA TACCAGGCCT CAACCAACGA     900

CTCCTGTGGA CCACCCTGAA TCCCGCCTCT GTGATGCAGT ATATGAAACA AAAGATGTCC     960
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10

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GAGGAAAAGA TCAGCTTCGA CTTCGAGACC GTGGAGCAGT ACATGAAGCG TGCGGCCATT      1020

GGCAGTGGCT ACATGGAGAA GCCCTGCCTG AACCCACTGA ATCCCAATTG CCCGGACACG      1080

GCACCGAACA AGAACAGCAC CCAGCCGCCG GATGTGGGAG CCATCCTGTC CGGAGGCTGC      1140

TACGGTTATG CCGCGAAGCA CATGCACTGG CCGGAGGAGC TGATTGTGGG CGGACGGAAG      1200

AGGAACCGCA GCGGACACTT GAGGAAGGCC CAGGCCCTGC AGTCGGTGGT GCAGCTGATG      1260

ACCGAGAAGG AAATGTACGA CCAGTGGCAG GACAACTACA AGGTGCACCA TCTTGGATGG      1320

ACGCAGGAGA AGGCAGCGGA GGTTTTGAAC GCCTGGCAGC GCAACTTTTC GCGGGAGGTG      1380

GAACAGCTGC TACGTAAACA GTCGAGAATT GCCACCAACT ACGATATCTA CGTGTTCAGC      1440

TCGGCTGCAC TGGATGACAT CCTGGCCAAG TTCTCCCATC CCAGCGCCTT GTCCATTGTC      1500

ATCGGCGTGG CCGTCACCGT TTTGTATGCC TTTTGCACGC TCCTCCGCTG GAGGGACCCC      1560

GTCCGTGGCC AGAGCAGTGT GGGCGTGGCC GGAGTTCTGC TCATGTGCTT CAGTACCGCC      1620

GCCGGATTGG GATTGTCAGC CCTGCTCGGT ATCGTTTTCA ATGCGCTGAC CGCTGCCTAT      1680

GCGGAGAGCA ATCGGCGGGA GCAGACCAAG CTGATTCTCA AGAACGCCAG CACCCAGGTG      1740

GTTCCGTTTT TGGCCCTTGG TCTGGGCGTC GATCACATCT TCATAGTGGG ACCGAGCATC      1800

CTGTTCAGTG CCTGCAGCAC CGCAGGATCC TTCTTTGCGG CCGCCTTTAT TCCGGTGCCG      1860

GCTTTGAAGG TATTCTGTCT GCAGGCTGCC ATCGTAATGT GCTCCAATTT GGCAGCGGCT      1920

CTATTGGTTT TTCCGGCCAT GATTTCGTTG GATCTACGGA GACGTACCGC CGGCAGGGCG      1980

GACATCTTCT GCTGCTGTTT TCCGGTGTGG AAGGAACAGC CGAAGGTGGC ACCTCCGGTG      2040

CTGCCGCTGA ACAACAACAA CGGGCGCGGG GCCCGGCATC CGAAGAGCTG CAACAACAAC      2100

AGGGTGCCGC TGCCCGCCCA GAATCCTCTG CTGGAACAGA GGGCAGACAT CCCTGGGAGC      2160

AGTCACTCAC TGGCGTCCTT CTCCCTGGCA ACCTTCGCCT TTCAGCACTA CACTCCCTTC      2220

CTCATGCGCA GCTGGGTGAA GTTCCTGACC GTTATGGGTT CCTGGCGGC CCTCATATCC      2280

AGCTTGTATG CCTCCACGCG CCTTCAGGAT GGCCTGGACA TTATTGATCT GGTGCCCAAG      2340

GACAGCAACG AGCACAAGTT CCTGGATGCT CAAACTCGGC TCTTTGGCTT CTACAGCATG      2400

TATGCGGTTA CCCAGGGCAA CTTTGAATAT CCCACCCAGC AGCAGTTGCT CAGGGACTAC      2460

CATGATTCCT TTGTGCGGGT GCCACATGTG ATCAAGAATG ATAACGGTGG ACTGCCGGAC      2520

TTCTGGCTGC TGCTCTTCAG CGAGTGGCTG GGTAATCTGC AAAAGATATT CGACGAGGAA      2580

TACCGCGACG GACGGCTGAC CAAGGAGTGC TGGTTCCCAA ACGCCAGCAG CGATGCCATC      2640

CTGGCCTACA AGCTAATCGT GCAAACCGGC CATGTGGACA ACCCCGTGGA CAAGGAACTG      2700
```

11

```
GTGCTCACCA ATCGCCTGGT CAACAGCGAT GGCATCATCA ACCAACGCGC CTTCTACAAC    2760

TATCTGTCGG CATGGGCCAC CAACGACGTC TTCGCCTACG GAGCTTCTCA GGGCAAATTG    2820

TATCCGGAAC CGCGCCAGTA TTTTCACCAA CCCAACGAGT ACGATCTTAA GATACCCAAG    2880

AGTCTGCCAT TGGTCTACGC TCAGATGCCC TTTTACCTCC ACGGACTAAC AGATACCTCG    2940

CAGATCAAGA CCCTGATAGG TCATATTCGC GACCTGAGCG TCAAGTACGA GGGCTTCGGC    3000

CTGCCCAACT ATCCATCGGG CATTCCCTTC ATCTTCTGGG AGCAGTACAT GACCCTGCGC    3060

TCCTCACTGG CCATGATCCT GGCCTGCGTG CTACTCGCCG CCCTGGTGCT GGTCTCCCTG    3120

CTCCTGCTCT CCGTTTGGGC CGCCGTTCTC GTGATCCTCA GCGTTCTGGC CTCGCTGGCC    3180

CAGATCTTTG GGGCCATGAC TCTGCTGGGC ATCAAACTCT CGGCCATTCC GGCAGTCATA    3240

CTCATCCTCA GCGTGGGCAT GATGCTGTGC TTCAATGTGC TGATATCACT GGGCTTCATG    3300

ACATCCGTTG GCAACCGACA GCGCCGCGTC CAGCTGAGCA TGCAGATGTC CCTGGGACCA    3360

CTTGTCCACG GCATGCTGAC CTCCGGAGTG GCCGTGTTCA TGCTCTCCAC GTCGCCCTTT    3420

GAGTTTGTGA TCCGGCACTT CTGCTGGCTT CTGCTGGTGG TCTTATGCGT TGGCGCCTGC    3480

AACAGCCTTT TGGTGTTCCC CATCCTACTG AGCATGGTGG ACCGGAGGC GGAGCTGGTG    3540

CCGCTGGAGC ATCCAGACCG CATATCCACG CCCTCTCCGC TGCCCGTGCG CAGCAGCAAG    3600

AGATCGGGCA AATCCTATGT GGTGCAGGGA TCGCGATCCT CGCGAGGCAG CTGCCAGAAG    3660

TCGCATCACC ACCACCACAA AGACCTTAAT GATCCATCGC TGACGACGAT CACCGAGGAG    3720

CCGCAGTCGT GGAAGTCCAG CAACTCGTCC ATCCAGATGC CCAATGATTG GACCTACCAG    3780

CCGCGGGAAC AGCGACCCGC CTCCTACGCG GCCCCGCCCC CCGCCTATCA CAAGGCCGCC    3840

GCCCAGCAGC ACCACCAGCA TCAGGGCCCG CCCACAACGC CCCCGCCTCC CTTCCCGACG    3900

GCCTATCCGC CGGAGCTGCA GAGCATCGTG GTGCAGCCGG AGGTGACGGT GGAGACGACG    3960

CACTCGGACA GCAACACCAC CAAGGTGACG GCCACGGCCA ACATCAAGGT GGAGCTGGCC    4020

ATGCCCGGCA GGGCGGTGCG CAGCTATAAC TTTACGAGTT AGCACTAGCA CTAGTTCCTG    4080

TAGCTATTAG GACGTATCTT TAGACTCTAG CCTAAGCCGT AACCCTATTT GTATCTGTAA    4140

AATCGATTTG TCCAGCGGGT CTGCTGAGGA TTTCGTTCTC ATGGATTCTC ATGGATTCTC    4200

ATGGATGCTT AAATGGCATG GTAATTGGCA AAATATCAAT TTTTGTGTCT CAAAAAGATG    4260

CATTAGCTTA TGGTTTCAAG ATACATTTTT AAAGAGTCCG CCAGATATTT ATATAAAAAA    4320

AATCCAAAAT CGACGTATCC ATGAAAATTG AAAAGCTAAG CAGACCCGTA TGTATGTATA    4380

TGTGTATGCA TGTTAGTTAA TTTCCCGAAG TCCGGTATTT ATAGCAGCTG CCTT          4434
```

(2) INFORMATION FOR SEQ ID NO:6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1286 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Met Asp Arg Asp Ser Leu Pro Arg Val Pro Asp Thr His Gly Asp Val
1               5               10              15

Val Asp Glu Lys Leu Phe Ser Asp Leu Tyr Ile Arg Thr Ser Trp Val
        20              25              30

Asp Ala Gln Val Ala Leu Asp Gln Ile Asp Lys Gly Lys Ala Arg Gly
        35              40              45

Ser Arg Thr Ala Ile Tyr Leu Arg Ser Val Phe Gln Ser His Leu Glu
    50              55              60

Thr Leu Gly Ser Ser Val Gln Lys His Ala Gly Lys Val Leu Phe Val
65              70              75              80

Ala Ile Leu Val Leu Ser Thr Phe Cys Val Gly Leu Lys Ser Ala Gln
                85              90              95

Ile His Ser Lys Val His Gln Leu Trp Ile Gln Glu Gly Gly Arg Leu
            100             105             110

Glu Ala Glu Leu Ala Tyr Thr Gln Lys Thr Ile Gly Glu Asp Glu Ser
        115             120             125

Ala Thr His Gln Leu Leu Ile Gln Thr Thr His Asp Pro Asn Ala Ser
    130             135             140

Val Leu His Pro Gln Ala Leu Leu Ala His Leu Glu Val Leu Val Lys
145             150             155             160

Ala Thr Ala Val Lys Val His Leu Tyr Asp Thr Glu Trp Gly Leu Arg
            165             170             175

Asp Met Cys Asn Met Pro Ser Thr Pro Ser Phe Glu Gly Ile Tyr Tyr
        180             185             190

Ile Glu Gln Ile Leu Arg His Leu Ile Pro Cys Ser Ile Ile Thr Pro
        195             200             205

Leu Asp Cys Phe Trp Glu Gly Ser Gln Leu Leu Gly Pro Glu Ser Ala
    210             215             220

Val Val Ile Pro Gly Leu Asn Gln Arg Leu Leu Trp Thr Thr Leu Asn
225             230             235             240
```

Pro Ala Ser Val Met Gln Tyr Met Lys Gln Lys Met Ser Glu Glu Lys
                    245   250   255

Ile Ser Phe Asp Phe Glu Thr Val Glu Gln Tyr Met Lys Arg Ala Ala
            260   265   270

Ile Gly Ser Gly Tyr Met Glu Lys Pro Cys Leu Asn Pro Leu Asn Pro
        275   280   285

Asn Cys Pro Asp Thr Ala Pro Asn Lys Asn Ser Thr Gln Pro Pro Asp
    290   295   300

Val Gly Ala Ile Leu Ser Gly Gly Cys Tyr Gly Tyr Ala Ala Lys His
305   310   315   320

Met His Trp Pro Glu Glu Leu Ile Val Gly Gly Arg Lys Arg Asn Arg
            325   330   335

Ser Gly His Leu Arg Lys Ala Gln Ala Leu Gln Ser Val Val Gln Leu
        340   345   350

Met Thr Glu Lys Glu Met Tyr Asp Gln Trp Gln Asp Asn Tyr Lys Val
        355   360   365

His His Leu Gly Trp Thr Gln Glu Lys Ala Ala Glu Val Leu Asn Ala
370   375   380

Trp Gln Arg Asn Phe Ser Arg Glu Val Glu Gln Leu Leu Arg Lys Gln
385   390   395   400

Ser Arg Ile Ala Thr Asn Tyr Asp Ile Tyr Val Phe Ser Ser Ala Ala
            405   410   415

Leu Asp Asp Ile Leu Ala Lys Phe Ser His Pro Ser Ala Leu Ser Ile
            420   425   430

Val Ile Gly Val Ala Val Thr Val Leu Tyr Ala Phe Cys Thr Leu Leu
        435   440   445

Arg Trp Arg Asp Pro Val Arg Gly Gln Ser Ser Val Gly Val Ala Gly
450   455   460

Val Leu Leu Met Cys Phe Ser Thr Ala Ala Gly Leu Gly Leu Ser Ala
465   470   475   480

Leu Leu Gly Ile Val Phe Asn Ala Leu Thr Ala Ala Tyr Ala Glu Ser
            485   490   495

Asn Arg Arg Glu Gln Thr Lys Leu Ile Leu Lys Asn Ala Ser Thr Gln
            500   505   510

Val Val Pro Phe Leu Ala Leu Gly Leu Gly Val Asp His Ile Phe Ile
        515   520   525

Val Gly Pro Ser Ile Leu Phe Ser Ala Cys Ser Thr Ala Gly Ser Phe
    530   535   540

Phe Ala Ala Ala Phe Ile Pro Val Pro Ala Leu Lys Val Phe Cys Leu

14

Gln Ala Ala Ile Val Met Cys Ser Asn Leu Ala Ala Ala Leu Leu Val
                565   570   575

Phe Pro Ala Met Ile Ser Leu Asp Leu Arg Arg Arg Thr Ala Gly Arg
                580   585   590

Ala Asp Ile Phe Cys Cys Cys Phe Pro Val Trp Lys Glu Gln Pro Lys
            595   600   605

Val Ala Pro Pro Val Leu Pro Leu Asn Asn Asn Asn Gly Arg Gly Ala
    610   615   620

Arg His Pro Lys Ser Cys Asn Asn Asn Arg Val Pro Leu Pro Ala Gln
625   630   635   640

Asn Pro Leu Leu Glu Gln Arg Ala Asp Ile Pro Gly Ser Ser His Ser
                645   650   655

Leu Ala Ser Phe Ser Leu Ala Thr Phe Ala Phe Gln His Tyr Thr Pro
                660   665   670

Phe Leu Met Arg Ser Trp Val Lys Phe Leu Thr Val Met Gly Phe Leu
                675   680   685

Ala Ala Leu Ile Ser Ser Leu Tyr Ala Ser Thr Arg Leu Gln Asp Gly
    690   695   700

Leu Asp Ile Ile Asp Leu Val Pro Lys Asp Ser Asn Glu His Lys Phe
705   710   715   720

Leu Asp Ala Gln Thr Arg Leu Phe Gly Phe Tyr Ser Met Tyr Ala Val
                725   730   735

Thr Gln Gly Asn Phe Glu Tyr Pro Thr Gln Gln Gln Leu Leu Arg Asp
                740   745   750

Tyr His Asp Ser Phe Val Arg Val Pro His Val Ile Lys Asn Asp Asn
                755   760   765

Gly Gly Leu Pro Asp Phe Trp Leu Leu Leu Phe Ser Glu Trp Leu Gly
    770   775   780

Asn Leu Gln Lys Ile Phe Asp Glu Glu Tyr Arg Asp Gly Arg Leu Thr
785   790   795   800

Lys Glu Cys Trp Phe Pro Asn Ala Ser Ser Asp Ala Ile Leu Ala Tyr
                805   810   815

Lys Leu Ile Val Gln Thr Gly His Val Asp Asn Pro Val Asp Lys Glu
            820   825   830

Leu Val Leu Thr Asn Arg Leu Val Asn Ser Asp Gly Ile Ile Asn Gln
            835   840   845

Arg Ala Phe Tyr Asn Tyr Leu Ser Ala Trp Ala Thr Asn Asp Val Phe
    850   855   860

15

Ala Tyr Gly Ala Ser Gln Gly Lys Leu Tyr Pro Glu Pro Arg Gln Tyr
865   870   875   880

Phe His Gln Pro Asn Glu Tyr Asp Leu Lys Ile Pro Lys Ser Leu Pro
              885   890   895

Leu Val Tyr Ala Gln Met Pro Phe Tyr Leu His Gly Leu Thr Asp Thr
          900   905   910

Ser Gln Ile Lys Thr Leu Ile Gly His Ile Arg Asp Leu Ser Val Lys
      915   920   925

Tyr Glu Gly Phe Gly Leu Pro Asn Tyr Pro Ser Gly Ile Pro Phe Ile
    930   935   940

Phe Trp Glu Gln Tyr Met Thr Leu Arg Ser Ser Leu Ala Met Ile Leu
945   950   955   960

Ala Cys Val Leu Leu Ala Ala Leu Val Leu Val Ser Leu Leu Leu. Leu
          965   970   975

Ser Val Trp Ala Ala Val Leu Val Ile Leu Ser Val Leu Ala Ser Leu
          980   985   990

Ala Gln Ile Phe Gly Ala Met Thr Leu Leu Gly Ile Lys Leu Ser Ala
      995   1000   1005

Ile Pro Ala Val Ile Leu Ile Leu Ser Val Gly Met Met Leu Cys Phe
    1010   1015   1020

Asn Val Leu Ile Ser Leu Gly Phe Met Thr Ser Val Gly Asn Arg Gln
1025   1030   1035   1040

Arg Arg Val Gln Leu Ser Met Gln Met Ser Leu Gly Pro Leu Val His
          1045   1050   1055

Gly Met Leu Thr Ser Gly Val Ala Val Phe Met Leu Ser Thr Ser Pro
          1060   1065   1070

Phe Glu Phe Val Ile Arg His Phe Cys Trp Leu Leu Leu Val Val Leu
          1075   1080   1085

Cys Val Gly Ala Cys Asn Ser Leu Leu Val Phe Pro Ile Leu Leu Ser
    1090   1095   1100

Met Val Gly Pro Glu Ala Glu Leu Val Pro Leu Glu His Pro Asp Arg
1105   1110   1115   1120

Ile Ser Thr Pro Ser Pro Leu Pro Val Arg Ser Ser Lys Arg Ser Gly
              1125   1130   1135

Lys Ser Tyr Val Val Gln Gly Ser Arg Ser Ser Arg Gly Ser Cys Gln
          1140   1145   1150

Lys Ser His His His His His Lys Asp Leu Asn Asp Pro Ser Leu Thr
          1155   1160   1165

Thr Ile Thr Glu Glu Pro Gln Ser Trp Lys Ser Ser Asn Ser Ser Ile

16

```
Gln Met Pro Asn Asp Trp Thr Tyr Gln Pro Arg Glu Gln Arg Pro Ala
1185             1190             1195             1200

Ser Tyr Ala Ala Pro Pro Pro Ala Tyr His Lys Ala Ala Ala Gln Gln
             1205             1210             1215

His His Gln His Gln Gly Pro Pro Thr Thr Pro Pro Pro Pro Phe Pro
         1220             1225             1230

Thr Ala Tyr Pro Pro Glu Leu Gln Ser Ile Val Val Gln Pro Glu Val
         1235             1240             1245

Thr Val Glu Thr Thr His Ser Asp Ser Asn Thr Thr Lys Val Thr Ala
         1250             1255             1260

Thr Ala Asn Ile Lys Val Glu Leu Ala Met Pro Gly Arg Ala Val Arg
1265             1270             1275             1280

Ser Tyr Asn Phe Thr Ser
                1285
```

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 342 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
AAGGTCCATC AGCTTTGGAT ACAGGAAGGT GGTTCGCTCG AGCATGAGCT AGCCTACACG      60

CAGAAATCGC TCGGCGAGAT GGACTCCTCC ACGCACCAGC TGCTAATCCA AACCCCAAAG     120

ATATGGACGC CTCGATACTG CACCCGAACG CGCTACTGAC GCACCTGGAC GTGGTGAAGA     180

AAGCGATCTC GGTGACGGTG CACATGTACG ACATCACGTG GAGCTCAAGG ACATGTGCTA     240

CTCGCCCAGC ATACCGAGTT CGATACGCAC TTTATCGAGC AGATCTTCGA GAACATCATA     300

CCGTGCGCGA TCATCACGCC GCTGGATTGC TTTTGGGAGG GA                        342
```

(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 115 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
Lys Val His Gln Leu Trp Ile Gln Glu Gly Gly Ser Leu Glu His Glu
1               5               10              15
Leu Ala Tyr Thr Gln Lys Ser Leu Gly Glu Met Asp Ser Ser Thr His
            20              25              30
Gln Leu Leu Ile Gln Thr Pro Lys Asp Met Asp Ala Ser Ile Leu His
        35              40              45
Pro Asn Ala Leu Leu Thr His Leu Asp Val Val Lys Lys Ala Ile Ser
    50              55              60
Val Thr Val His Met Tyr Asp Ile Thr Trp Xaa Leu Lys Asp Met Cys
65              70              75              80
Tyr Ser Pro Ser Ile Pro Xaa Phe Asp Thr His Phe Ile Glu Gln Ile
            85              90              95
Phe Glu Asn Ile Ile Pro Cys Ala Ile Ile Thr Pro Leu Asp Cys Phe
            100             105             110
Trp Glu Gly
    115
```

(2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGATGTTAAT ATTCTCATCG   20

(2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1356 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

18

Met Ala Ser Ala Gly Asn Ala Arg Arg Gly Pro Gly Gln Ala Gly Arg
1   5   10   15

Arg Arg Glu Ala Gln Thr Asp Arg Gly Thr Ala Pro Arg Arg Ala Gly
            20   25   30

Pro Gly Leu Ser Ala Pro Ala Gln Leu Leu Arg Arg Ala Phe Ala Leu
        35   40   45

Glu Gln Ile Ser Lys Gly Lys Ala Thr Gly Arg Lys Ala Pro Leu Trp
    50   55   60

Leu Arg Ala Lys Phe Gln Arg Leu Leu Phe Lys Leu Gly Cys Tyr Ile
65   70   75   80

Gln Lys Asn Cys Gly Lys Phe Leu Val Val Gly Leu Leu Ile Phe Gly
            85   90   95

Ala Phe Ala Val Gly Leu Lys Ala Ala Asn Leu Glu Thr Asn Val Glu
            100   105   110

Glu Leu Trp Val Glu Val Gly Gly Arg Val Ser Arg Glu Leu Asn Tyr
        115   120   125

Thr Arg Gln Lys Ile Gly Glu Glu Ala Met Phe Asn Pro Gln Leu Met
    130   135   140

Ile Gln Thr Pro Lys Glu Glu Gly Ala Asn Val Leu Thr Thr Glu Ala
145   150   155   160

Leu Leu Gln His Leu Asp Ser Ala Leu Gln Ala Ser Arg Val His Val
            165   170   175

Tyr Met Tyr Asn Arg Gln Trp Lys Leu Glu His Leu Cys Tyr Lys Ser
            180   185   190

Gly Glu Leu Ile Thr Glu Thr Gly Tyr Met Asp Gln Ile Ile Glu Tyr
        195   200   205

Leu Tyr Pro Cys Leu Ile Ile Thr Pro Leu Asp Cys Phe Trp Glu Gly
    210   215   220

Ala Lys Leu Gln Ser Gly Thr Ala Tyr Leu Leu Gly Lys Pro Pro Leu
225   230   235   240

Arg Trp Thr Asn Phe Asp Pro Leu Glu Phe Leu Glu Glu Leu Lys Lys
            245   250   255

Ile Asn Tyr Gln Val Asp Ser Trp Glu Glu Met Leu Asn Lys Ala Glu
        260   265   270

Val Gly His Gly Tyr Met Asp Arg Pro Cys Leu Asn Pro Ala Asp Pro
    275   280   285

Asp Cys Pro Ala Thr Ala Pro Asn Lys Asn Ser Thr Lys Pro Leu Asp
290   295   300

Val Ala Leu Val Leu Asn Gly Gly Cys Gln Gly Leu Ser Arg Lys Tyr

Met His Trp Gln Glu Glu Leu Ile Val Gly Gly Thr Val Lys Asn Ala
            325   330   335

Thr Gly Lys Leu Val Ser Ala His Ala Leu Gln Thr Met Phe Gln Leu
            340   345   350

Met Thr Pro Lys Gln Met Tyr Glu His Phe Arg Gly Tyr Asp Tyr Val
            355   360   365

Ser His Ile Asn Trp Asn Glu Asp Arg Ala Ala Ala Ile Leu Glu Ala
370   375   380

Trp Gln Arg Thr Tyr Val Glu Val Val His Gln Ser Val Ala Pro Asn
385   390   395   400

Ser Thr Gln Lys Val Leu Pro Phe Thr Thr Thr Thr Leu Asp Asp Ile
            405   410   415

Leu Lys Ser Phe Ser Asp Val Ser Val Ile Arg Val Ala Ser Gly Tyr
            420   425   430

Leu Leu Met Leu Ala Tyr Ala Cys Leu Thr Met Leu Arg Trp Asp Cys
            435   440   445

Ser Lys Ser Gln Gly Ala Val Gly Leu Ala Gly Val Leu Leu Val Ala
            450   455   460

Leu Ser Val Ala Ala Gly Leu Gly Leu Cys Ser Leu Ile Gly Ile Ser
465   470   475   480

Phe Asn Ala Ala Thr Thr Gln Val Leu Pro Phe Leu Ala Leu Gly Val
            485   490   495

Gly Val Asp Asp Val Phe Leu Leu Ala His Ala Phe Ser Glu Thr Gly
            500   505   510

Gln Asn Lys Arg Ile Pro Phe Glu Asp Arg Thr Gly Glu Cys Leu Lys
            515   520   525

Arg Thr Gly Ala Ser Val Ala Leu Thr Ser Ile Ser Asn Val Thr Ala
            530   535   540

Phe Phe Met Ala Ala Leu Ile Pro Ile Pro Ala Leu Arg Ala Phe Ser
545   550   555   560

Leu Gln Ala Ala Val Val Val Phe Asn Phe Ala Met Val Leu Leu
            565   570   575

Ile Phe Pro Ala Ile Leu Ser Met Asp Leu Tyr Arg Arg Glu Asp Arg
            580   585   590

Arg Leu Asp Ile Phe Cys Cys Leu Thr Ser Pro Cys Val Ser Arg Val
            595   600   605

Ile Gln Val Glu Pro Gln Ala Tyr Thr Glu Pro His Ser Asn Thr Arg
            610   615   620

Tyr Ser Pro Pro Pro Pro Tyr Thr Ser His Ser Phe Ala His Glu Thr
625   630   635   640

His Ile Thr Met Gln Ser Thr Val Gln Leu Arg Thr Glu Tyr Asp Pro
              645   650   655

His Thr His Val Tyr Tyr Thr Thr Ala Glu Pro Arg Ser Glu Ile Ser
              660   665   670

Val Gln Pro Val Thr Val Thr Gln Asp Asn Leu Ser Cys Gln Ser Pro
          675   680   685

Glu Ser Thr Ser Ser Thr Arg Asp Leu Leu Ser Gln Phe Ser Asp Ser
    690   695   700

Ser Leu His Cys Leu Glu Pro Pro Cys Thr Lys Trp Thr Leu Ser Ser
705   710   715   720

Phe Ala Glu Lys His Tyr Ala Pro Phe Leu Leu Lys Pro Lys Ala Lys
              725   730   735

Val Val Val Ile Leu Leu Phe Leu Gly Leu Leu Gly Val Ser Leu Tyr
              740   745   750

Gly Thr Thr Arg Val Arg Asp Gly Leu Asp Leu Thr Asp Ile Val Pro
    755   760   765

Arg Glu Thr Arg Glu Tyr Asp Phe Ile Ala Ala Gln Phe Lys Tyr Phe
    770   775   780

Ser Phe Tyr Asn Met Tyr Ile Val Thr Gln Lys Ala Asp Tyr Pro Asn
785   790   795   800

Ile Gln His Leu Leu Tyr Asp Leu His Lys Ser Phe Ser Asn Val Lys
              805   810   815

Tyr Val Met Leu Glu Glu Asn Lys Gln Leu Pro Gln Met Trp Leu His
          820   825   830

Tyr Phe Arg Asp Trp Leu Gln Gly Leu Gln Asp Ala Phe Asp Ser Asp
        835   840   845

Trp Glu Thr Gly Arg Ile Met Pro Asn Asn Tyr Lys Asn Gly Ser Asp
    850   855   860

Asp Gly Val Leu Ala Tyr Lys Leu Leu Val Gln Thr Gly Ser Arg Asp
865   870   875   880

Lys Pro Ile Asp Ile Ser Gln Leu Thr Lys Gln Arg Leu Val Asp Ala
              885   890   895

Asp Gly Ile Ile Asn Pro Ser Ala Phe Tyr Ile Tyr Leu Thr Ala Trp
              900   905   910

Val Ser Asn Asp Pro Val Ala Tyr Ala Ala Ser Gln Ala Asn Ile Arg
    915   920   925

Pro His Arg Pro Glu Trp Val His Asp Lys Ala Asp Tyr Met Pro Glu

21

```
              930                   935                   940
Thr Arg Leu Arg Ile Pro Ala Ala Glu Pro Ile Glu Tyr Ala Gln Phe
945                 950                 955                 960

Pro Phe Tyr Leu Asn Gly Leu Arg Asp Thr Ser Asp Phe Val Glu Ala
                965                 970                 975

Ile Glu Lys Val Arg Val Ile Cys Asn Asn Tyr Thr Ser Leu Gly Leu
                980                 985                 990

Ser Ser Tyr Pro Asn Gly Tyr Pro Phe Leu Phe Trp Glu Gln Tyr Ile
                995                 1000                1005

Ser Leu Arg His Trp Leu Leu Leu Ser Ile Ser Val Val Leu Ala Cys
          1010                1015                1020

Thr Phe Leu Val Cys Ala Val Phe Leu Leu Asn Pro Trp Thr Ala Gly
1025                1030                1035                1040

Ile Ile Val Met Val Leu Ala Leu Met Thr Val Glu Leu Phe Gly Met
                1045                1050                1055

Met Gly Leu Ile Gly Ile Lys Leu Ser Ala Val Pro Val Val Ile Leu
          1060                1065                1070

Ile Ala Ser Val Gly Ile Gly Val Glu Phe Thr Val His Val Ala Leu
          1075                1080                1085

Ala Phe Leu Thr Ala Ile Gly Asp Lys Asn His Arg Ala Met Leu Ala
          1090                1095                1100

Leu Glu His Met Phe Ala Pro Val Leu Asp Gly Ala Val Ser Thr Leu
1105                1110                1115                1120

Leu Gly Val Leu Met Leu Ala Gly Ser Glu Phe Asp Phe Ile Val Arg
                1125                1130                1135

Tyr Phe Phe Ala Val Leu Ala Ile Leu Thr Val Leu Gly Val Leu Asn
                1140                1145                1150

Gly Leu Val Leu Leu Pro Val Leu Leu Ser Phe Phe Gly Pro Cys Pro
          1155                1160                1165

Glu Val Ser Pro Ala Asn Gly Leu Asn Arg Leu Pro Thr Pro Ser Pro
          1170                1175                1180

Glu Pro Pro Pro Ser Val Val Arg Phe Ala Val Pro Pro Gly His Thr
1185                1190                1195                1200

Asn Asn Gly Ser Asp Ser Ser Asp Ser Glu Tyr Ser Ser Gln Thr Thr
                1205                1210                1215

Val Ser Gly Ile Ser Glu Glu Leu Arg Gln Tyr Glu Ala Gln Gln Gly
          1220                1225                1230

Ala Gly Gly Pro Ala His Gln Val Ile Val Glu Ala Thr Glu Asn Pro
          1235                1240                1245
```

22

```
Val Phe Ala Arg Ser Thr Val Val His Pro Asp Ser Arg His Gln Pro
    1250                1255            1260
```

```
Pro Leu Thr Pro Arg Gln Gln Pro His Leu Asp Ser Gly Ser Leu Ser
    1265            1270                1275                1280
```

```
Pro Gly Arg Gln Gly Gln Gln Pro Arg Arg Asp Pro Pro Arg Glu Gly
                1285                1290                1295
```

```
Leu Arg Pro Pro Pro Tyr Arg Pro Arg Arg Asp Ala Phe Glu Ile Ser
                1300            1305                1310
```

```
Thr Glu Gly His Ser Gly Pro Ser Asn Arg Asp Arg Ser Gly Pro Val
        1315                1320                1325
```

```
Gly Pro Val Leu Thr Thr Leu Gly Thr Gln Arg Pro Pro Pro Trp Ala
    1330                1335                1340
```

```
Ala Leu Cys Pro Ala Thr Ala Ser Pro Ser Pro Leu
    1345                1350                1355
```

(2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1356 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
Met Ala Ser Ala Gly Asn Ala Arg Arg Gly Pro Gly Gln Ala Gly Arg
1               5               10                  15
```

```
Arg Arg Glu Ala Gln Thr Asp Arg Gly Thr Ala Pro Arg Arg Ala Gly
            20              25                  30
```

```
Pro Gly Leu Ser Ala Pro Ala Gln Leu Leu Arg Arg Ala Phe Ala Leu
        35              40                  45
```

```
Glu Gln Ile Ser Lys Gly Lys Ala Thr Gly Arg Lys Ala Pro Leu Trp
    50              55                  60
```

```
Leu Arg Ala Lys Phe Gln Arg Leu Leu Phe Lys Leu Gly Cys Tyr Ile
65              70                  75                      80
```

```
Gln Lys Asn Cys Gly Lys Phe Leu Val Val Gly Leu Leu Ile Phe Gly
            85                  90                      95
```

```
Ala Phe Ala Val Gly Leu Lys Ala Ala Asn Leu Glu Thr Asn Val Glu
            100             105                 110
```

```
Glu Leu Trp Val Glu Val Gly Gly Arg Val Ser Arg Glu Leu Asn Tyr
        115                 120                 125
```

23

```
Thr Arg Gln Lys Ile Gly Glu Glu Ala Met Phe Asn Pro Gln Leu Met
    130             135             140
Ile Gln Thr Pro Lys Glu Glu Gly Ala Asn Val Leu Thr Thr Glu Ala
145             150             155             160
Leu Leu Gln His Leu Asp Ser Ala Leu Gln Ala Ser Arg Val His Val
            165             170             175
Tyr Met Tyr Asn Arg Gln Trp Lys Leu Glu His Leu Cys Tyr Lys Ser
        180             185             190
Gly Glu Leu Ile Thr Glu Thr Gly Tyr Met Asp Gln Ile Ile Glu Tyr
        195             200             205
Leu Tyr Pro Cys Leu Ile Ile Thr Pro Leu Asp Cys Phe Trp Glu Gly
    210             215             220
Ala Lys Leu Gln Ser Gly Thr Ala Tyr Leu Leu Gly Lys Pro Pro Leu
225             230             235             240
Arg Trp Thr Asn Phe Asp Pro Leu Glu Phe Leu Glu Glu Leu Lys Lys
            245             250             255
Ile Asn Tyr Gln Val Asp Ser Trp Glu Glu Met Leu Asn Lys Ala Glu
        260             265             270
Val Gly His Gly Tyr Met Asp Arg Pro Cys Leu Asn Pro Ala Asp Pro
    275             280             285
Asp Cys Pro Ala Thr Ala Pro Asn Lys Asn Ser Thr Lys Pro Leu Asp
    290             295             300
Val Ala Leu Val Leu Asn Gly Gly Cys Gln Gly Leu Ser Arg Lys Tyr
305             310             315             320
Met His Trp Gln Glu Glu Leu Ile Val Gly Gly Thr Val Lys Asn Ala
            325             330             335
Thr Gly Lys Leu Val Ser Ala His Ala Leu Gln Thr Met Phe Gln Leu
            340             345             350
Met Thr Pro Lys Gln Met Tyr Glu His Phe Arg Gly Tyr Asp Tyr Val
        355             360             365
Ser His Ile Asn Trp Asn Glu Asp Arg Ala Ala Ala Ile Leu Glu Ala
    370             375             380
Trp Gln Arg Thr Tyr Val Glu Val Val His Gln Ser Val Ala Pro Asn
385             390             395             400
Ser Thr Gln Lys Val Leu Pro Phe Thr Thr Thr Thr Leu Asp Asp Ile
            405             410             415
Leu Lys Ser Phe Ser Asp Val Ser Val Ile Arg Val Ala Ser Gly Tyr
            420             425             430
Leu Leu Met Leu Ala Tyr Ala Cys Leu Thr Met Leu Arg Trp Asp Cys
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          435                    440                    445
Ser Lys Ser Gln Gly Ala Val Gly Leu Ala Gly Val Leu Leu Val Ala
    450             455             460
Leu Ser Val Ala Ala Gly Leu Gly Leu Cys Ser Leu Ile Gly Ile Ser
465             470             475             480
Phe Asn Ala Ala Thr Thr Gln Val Leu Pro Phe Leu Ala Leu Gly Val
                485             490                 495
Gly Val Asp Asp Val Phe Leu Leu Ala His Ala Phe Ser Glu Thr Gly
            500             505             510
Gln Asn Lys Arg Ile Pro Phe Glu Asp Arg Thr Gly Glu Cys Leu Lys
        515             520             525
Arg Thr Gly Ala Ser Val Ala Leu Thr Ser Ile Ser Asn Val Thr Ala
    530             535             540    •
Phe Phe Met Ala Ala Leu Ile Pro Ile Pro Ala Leu Arg Ala Phe Ser
545             550             555             560
Leu Gln Ala Ala Val Val Val Val Phe Asn Phe Ala Met Val Leu Leu
            565             570             575
Ile Phe Pro Ala Ile Leu Ser Met Asp Leu Tyr Arg Arg Glu Asp Arg
        580         .   585             590
Arg Leu Asp Ile Phe Cys Cys Leu Thr Ser Pro Cys Val Ser Arg Val
        595             600             605
Ile Gln Val Glu Pro Gln Ala Tyr Thr Glu Pro His Ser Asn Thr Arg
    610             615             620
Tyr Ser Pro Pro Pro Pro Tyr Thr Ser His Ser Phe Ala His Glu Thr
625             630             635             640
His Ile Thr Met Gln Ser Thr Val Gln Leu Arg Thr Glu Tyr Asp Pro
            645             650             655
His Thr His Val Tyr Tyr Thr Thr Ala Glu Pro Arg Ser Glu Ile Ser
            660             665             670
Val Gln Pro Val Thr Val Thr Gln Asp Asn Leu Ser Cys Gln Ser Pro
        675             680             685
Glu Ser Thr Ser Ser Thr Arg Asp Leu Leu Ser Gln Phe Ser Asp Ser
    690             695             700
Ser Leu His Cys Leu Glu Pro Pro Cys Thr Lys Trp Thr Leu Ser Ser
705             710             715             720
Phe Ala Glu Lys His Tyr Ala Pro Phe Leu Leu Lys Pro Lys Ala Lys
            725             730             735
Val Val Val Ile Leu Leu Phe Leu Gly Leu Leu Gly Val Ser Leu Tyr
            740             745             750
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Gly Thr Thr Arg Val Arg Asp Gly Leu Asp Leu Thr Asp Ile Val Pro
        755   760   765

Arg Glu Thr Arg Glu Tyr Asp Phe Ile Ala Ala Gln Phe Lys Tyr Phe
        770   775   780

Ser Phe Tyr Asn Met Tyr Ile Val Thr Gln Lys Ala Asp Tyr Pro Asn
785   790   795   800

Ile Gln His Leu Leu Tyr Asp Leu His Lys Ser Phe Ser Asn Val Lys
                805   810   815

Tyr Val Met Leu Glu Glu Asn Lys Gln Leu Pro Gln Met Trp Leu His
            820   825   830

Tyr Phe Arg Asp Trp Leu Gln Gly Leu Gln Asp Ala Phe Asp Ser Asp
        835   840   845

Trp Glu Thr Gly Arg Ile Met Pro Asn Asn Tyr Lys Asn Gly Ser Asp
    850   855   860

Asp Gly Val Leu Ala Tyr Lys Leu Leu Val Gln Thr Gly Ser Arg Asp
865   870   875   880

Lys Pro Ile Asp Ile Ser Gln Leu Thr Lys Gln Arg Leu Val Asp Ala
            885   890   895

Asp Gly Ile Ile Asn Pro Ser Ala Phe Tyr Ile Tyr Leu Thr Ala Trp
            900   905   910

Val Ser Asn Asp Pro Val Ala Tyr Ala Ala Ser Gln Ala Asn Ile Arg
    915   920   925

Pro His Arg Pro Glu Trp Val His Asp Lys Ala Asp Tyr Met Pro Glu
    930   935   940

Thr Arg Leu Arg Ile Pro Ala Ala Glu Pro Ile Glu Tyr Ala Gln Phe
945   950   955   960

Pro Phe Tyr Leu Asn Gly Leu Arg Asp Thr Ser Asp Phe Val Glu Ala
                965   970   975

Ile Glu Lys Val Arg Val Ile Cys Asn Asn Tyr Thr Ser Leu Gly Leu
            980   985   990

Ser Ser Tyr Pro Asn Gly Tyr Pro Phe Leu Phe Trp Glu Gln Tyr Ile
        995   1000   1005

Ser Leu Arg His Trp Leu Leu Leu Ser Ile Ser Val Val Leu Ala Cys
    1010   1015   1020

Thr Phe Leu Val Cys Ala Val Phe Leu Leu Asn Pro Trp Thr Ala Gly
1025   1030   1035   1040

Ile Ile Val Met Val Leu Ala Leu Met Thr Val Glu Leu Phe Gly Met
            1045   1050   1055

Met Gly Leu Ile Gly Ile Lys Leu Ser Ala Val Pro Val Val Ile Leu

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                1060                    1065                    1070

    Ile Ala Ser Val Gly Ile Gly Val Glu Phe Thr Val His Val Ala Leu
                1075                    1080                    1085

    Ala Phe Leu Thr Ala Ile Gly Asp Lys Asn His Arg Ala Met Leu Ala
                1090                    1095                    1100

    Leu Glu His Met Phe Ala Pro Val Leu Asp Gly Ala Val Ser Thr Leu
    1105                    1110                    1115                    1120

    Leu Gly Val Leu Met Leu Ala Gly Ser Glu Phe Asp Phe Ile Val Arg
                1125                    1130                    1135

    Tyr Phe Phe Ala Val Leu Ala Ile Leu Thr Val Leu Gly Val Leu Asn
                1140                    1145                    1150

    Gly Leu Val Leu Leu Pro Val Leu Leu Ser Phe Phe Gly Pro Cys Pro
                1155                    1160                    1165

    Glu Val Ser Pro Ala Asn Gly Leu Asn Arg Leu Pro Thr Pro Ser Pro
                1170                    1175                    1180

    Glu Pro Pro Pro Ser Val Val Arg Phe Ala Val Pro Pro Gly His Thr
    1185                    1190                    1195                    1200

    Asn Asn Gly Ser Asp Ser Ser Asp Ser Glu Tyr Ser Ser Gln Thr Thr
                1205                    1210                    1215

    Val Ser Gly Ile Ser Glu Glu Leu Arg Gln Tyr Glu Ala Gln Gln Gly
                1220                    1225                    1230

    Ala Gly Gly Pro Ala His Gln Val Ile Val Glu Ala Thr Glu Asn Pro
                1235                    1240                    1245

    Val Phe Ala Arg Ser Thr Val Val His Pro Asp Ser Arg His Gln Pro
                1250                    1255                    1260

    Pro Leu Thr Pro Arg Gln Gln Pro His Leu Asp Ser Gly Ser Leu Ser
    1265                    1270                    1275                    1280

    Pro Gly Arg Gln Gly Gln Gln Pro Arg Arg Asp Pro Pro Arg Glu Gly
                1285                    1290                    1295

    Leu Arg Pro Pro Pro Tyr Arg Pro Arg Arg Asp Ala Phe Glu Ile Ser
                1300                    1305                    1310

    Thr Glu Gly His Ser Gly Pro Ser Asn Arg Asp Arg Ser Gly Pro Val
                1315                    1320                    1325

    Gly Pro Val Leu Thr Thr Leu Gly Thr Gln Arg Pro Pro Pro Trp Ala
                1330                    1335                    1340

    Ala Leu Cys Pro Ala Thr Ala Ser Pro Ser Pro Leu
    1345                    1350                    1355

(2)  INFORMATION FOR SEQ ID NO:12:
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(i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 9042 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GATCCTGAAT TGAGAAATAT AGATTGAAAC AGAATTCATT ACCATTTAAG CAATCATTAT   60

TTATGGGGGC GTAATGCGCC TCCGAGTAGG CAATGCTTTT CTTGACATTG TTACTAAGAA   120

TTGTGAATGA TATTTGGGCG TGGATCAACG CCGATTAAAA GCTGCTTTTG CTTCCAGGCG   180

GCCAGAGAAG AGATCCAAAC TTCAACTCCA GCCATAAAAG CAACAACATT TCCGTCTCCC   240

CCTTGTAGCT CCCCTTCCTC CGGCTCTTCC ACTCTCCACG AAACGGCAAA TGAAGCTCTC   300

AAAGCGAACT GTGCTTCGCT GGTGGTCCAT TGGCAGCTGC CGCCACACAG GCGCTGCTTT   360

TGTGTGTGTG TGTAATATCA ATCTTGCTCT CCCTCTCTTT TTATCTCTCT TGGGAATTGG   420

AGCTGCATGC GAATTGAGCG ACAGCAAAAC GAACTGCAAG TCATTGAGAG GAGAGCAAAA   480

ACTCGAGCGC AAGCCAAAGA TAGCGCAATC TGGGGAGAGC GAAATAAAGC TAAAATATGC   540

ATGTTGGAGA AAAAATGCCG CCCATGTCGC CAAAATGCGC CACACGCAGA GTGAGCGGGC   600

GGAGGTGGGA GTAATGGAAA GGGCGATGAG GAACGATTA GCTTGAAGAG AGAGAACAAC   660

AAATGAATGT GCTGCAACGT TAGTTCAGGT GAGCGCGTTA GAGAGAGAGT TGTTGTTTTT   720

TGATTGTAAT AGCTCGCTTG GTGGTGGGTC CACATTCACA TCTCCCTCTC CCACTCTTTC   780

TCCCCGAAAG AGAGAGCGGG AGCGAAGGGG CACGAGGGGA GCACGATGAC TATGCAGTTG   840

CATTCAATTT GAATTTCCAT GGTGCTGATG ATTCGAGCGC CAATTTTTTC GAAGAGTTCT   900

TATTTGTTTA CTTCGTTGTT GTTGCCTCAA TTGGAAAGGG AAAATGTGGA ATGCGGAGAA   960

ACACCAGAAG CAAATGCATT TCCATTCATA AATCCAAAGA AGTTTTAAAG ATAACATGTC   1020

ATTTGGCTTA AGTTCGTGGT GCACAAAAAA GATCGGTTTG CGGTTGTCGC ATGAAATGAG   1080

TTTATTCCAT TGGTATATTA TTATTCAGAA ATTAAAAAAA AACTTGTTTA GTCTATTTTT   1140

TTTTTTTAAA TAAAAAAAAA AAATTCTTTT ATAAGTCGAT TTTAGAGTAA ATATTTAAAG   1200

ACTACGTCTA ATAAACATAT AATTTGTTCT GTGTTTTAAT TTGCCGGCAA AAACAAACCT   1260

ACTTGTGTGG TCCTCGCACA CTCATAACCC CTCGCATATT TGAGATTCAT GGGGCAAGAG   1320

GCTGCAAAAA CAATGGAAAG GGAAAAGCAG AAACATCCTG CCGCTCATAA TTTAGCATCG   1380

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GAACATGCAA AAACAGACAT CATCGCATGG GGCAGCAGCA ACAGCCATAA AACCAACACG    1440

AGCAATGTAA AGCTAACAAA TTTGCCAACA GTTCGCGGCA CGGCTACACA CACACACATG    1500

CATGCGCAGC CTGCCACGCA CGCGCTTCCC CCAAACAAAT ACACACACAC ACACTGAGAC    1560

GAAAGCTCCA TTGGGCAGCG CTGCCGACGC TGAAGGCCGA CATCGGCAGA GCTGAACGTT    1620

TGGGTAGGGG ACCACCCACA TCGCTTGGCG GTTTCAGTTT AATGAAGGCA GAAACAAATT    1680

TATTTTTGGG TGGTCCACAC TGCAGCGAAA ATAAACTACA GTGGCAACAA CAAACCAGCA    1740

GCCAAGGCAC TTTGGGTGGT CCATGCAAAA AAAAAACAAA TTACGGCATG CGAATAACAA    1800

TAGAAATTAG CGCTCTCGTG GCGGAGCTAT TTGGGTATAT TAGAGCTACA TATTTTATTT    1860

GTTTATAAAA AGTATAAATG TAAACAATGA GTTCCAAGCA TTAAGTCCGT ATGCTCAACA    1920

ATTACATTAT CATTATTATT ATCACTTAAA TATTTACAAA GGATATTTAA ACAGTAATAG    1980

ATATATATTT TATTTCTTAA TTTCTGTTAA CATATGTATT TACATTGGTA GTTATTCTTT    2040

ATTTTGCAAC AAGCATTCAT AAATTTTATA TAACAAACTT GGTATTTTCT CGGAAAAACT    2100

CCTGAATCAC CCCTCGGTAT TTTGTGCGTT GAGCTATCGT TAAAGCAGCC CTCGCAGAGA    2160

GCGTTCTCAA ACCAAAATGG CCGCACACGA AACAAGAGAG CGAGTGAGAG TAGGGAGAGC    2220

GTCTGTGTTG TGTGTTGAGT GTCGCCCACG CACACAGGCG CAAAACAGTG CACACAGACG    2280

CCCGCTGGGC AAGAGAGAGT GAGAGAGAGA AACAGCGGCG CGCGCTCGCC TAATGAAGTT    2340

GTTGGCCTGG CTGGCGTGCC GCATCCACGA GATACAGATA CATCTCTCAG ACTGCGTGCG    2400

ATCCTCGAAC GAAACGGTTG TAAGTGCGGA GCGCGACGAC TTGTTATTCG TATTTCCGAC    2460

TACTGGCACT CTCTGTGTGT GGTATACTAA CAAGATAGAT ATCACAGAAC TCGTGGAAAA    2520

GCTAAGATAT TGTACCTCAC GGATGCGAGG CGAAGTTCAT GGATTAAATG CCAGGCAACA    2580

ACAAAAGCCA GCCAACCAGC CAGTGTTTGT GTGTGTGCGT CGCCAAGTGC AAAGTAAAGT    2640

AAAGGTAAAA GAGCGAAAGG CGAGAGAGAA AACCGAATAC GTGAGTCGTC CGACTGCCGC    2700

TTTTCCATGT GTAAAGATC TGTGAAAATT CTGTCAAATT CCCCTGAGAA ATTGTGCCCA    2760

AGATAAAACC CGAAAACCGC GTTTTAATCG TCGAAAAAAC CCAGCAAAAG CGAAGCCAGC    2820

AATCACAACA AAACAACATA ACGAGAGCTC AGATACACAG CGTGCTCAGT GAGTGAGCGA    2880

GAGAGCGCGG GAGAGAGCGT CTCTTGATTT AAAATACAAA ATAATTAAAA ATAAAAATGC    2940

GGAATGCAGT GCAAAATGCA GCCAAACAAA ATACGAGATT CCAATAACAA TTAATCGAAC    3000

CGAAAGTCCA CGAACAATCC GCACACTGTC TCCCAAGTCT CAGTTCTCAG GACGCAGACG    3060

AACGGCAGGC ACTGTAGAAA GACCGATTCC GCAGCACACT CCCATCTGCA CATCTCCGCC    3120
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ACGCGATTCC GTCCGGAATC TGGCTATAAA CATAACCATA ATGGACCGCG ACAGCCTCCC   3180

ACGCGTTCCG GACACACACG GCGATGTGGT CGATGAGAAA TTATTCTCGG ATCTTTACAT   3240

ACGCACCAGC TGGGTGGACG CCCAAGTGGC GCTCGATCAG ATAGATAAGG TGAGTGCCCA   3300

ACTACAGTGA ACTTTCACTG TGAAGGATAG CCATGTGTTG AATTCAATAA TATTCTTGAT   3360

CGTATTCGGA GGATCCAATT TTAATGCGTA TTTTATGGCA GTGGAGCAAG GCGGGGGAAT   3420

CTAAAAAAAA AACTAAACGC TAAATTCCGT ATTTTTGTTG CATTTTTCAG GGCAAAGCGC   3480

GTGGCAGCCG CACGGCGATC TATCTGCGAT CAGTATTCCA GTCCCACCTC GAAACCCTCG   3540

GCAGCTCCGT GCAAAAGCAC GCGGGCAAGG TGCTATTCGT GGCTATCCTG GTGCTGAGCA   3600

CCTTCTGCGT CGGCCTGAAG AGCGCCCAGA TCCACTCCAA GGTGCACCAG CTGTGGATCC   3660

AGGAGGGCGG CCGGCTGGAG GCGGAACTGG CCTACACACA GAAGACGATC GGCGAGGACG   3720

AGTCGGCCAC GCATCAGCTG CTCATTCAGA CGACCCACGA CCCGAACGCC TCCGTCCTGC   3780

ATCCGCAGGC GCTGCTTGCC CACCTGGAGG TCCTGGTCAA GGCCACCGCC GTCAAGGTGC   3840

ACCTCTACGA CACCGAATGG GGGCTGCGCG ACATGTGCAA CATGCCGAGC ACGCCCTCCT   3900

TCGAGGGCAT CTACTACATC GAGCAGATCC TGCGCCACCT CATTCCGTGC TCGATCATCA   3960

CGCCGCTGGA CTGTTTCTGG GAGGGAAGCC AGCTGTTGGG TCCGGAATCA GCGGTCGTTA   4020

TACCGTAAGT AGTTAATATG TAGTTAATAG CCACATCTTA TAGATTCTAA AGTGAACGTA   4080

TCCCTTATGA CCATATCCTT TTGCATGATC TACTTTAACC CACAGTACTT CTCTATTCAT   4140

ATTAAGGAAT TAATAAAGTA CTTACTTTGC GCTTACCTTT ATTAAATACG ATAGCTTATC   4200

TTTATAAACT TGCTATCAAG TCGAAAGATA AACGTGACAA GAGTATCTTT GTACTTATCC   4260

CAGTTGCTTA CCATCGTAAA TAATCTTCTT ATTAATAAAT ATTCGTAAAT AAATATTCTT   4320

AACTCAACAA ATCCATCTTT ATTATTGTTA CTCCTCTACA GAGGCCTCAA CCAACGACTC   4380

CTGTGGACCA CCCTGAATCC CGCCTCTGTG ATGCAGTATA TGAAACAAAA GATGTCCGAG   4440

GAAAAGATCA GCTTCGACTT CGAGACCGTG GAGCAGTACA TGAAGCGTGC GGCCATTGGC   4500

AGTGGCTACA TGGAGAAGCC CTGCCTGAAC CCACTGAATC CCAATTGCCC GGACACGGCA   4560

CCGAACAAGA ACAGCACCCA GCCGCCGGAT GTGGGAGCCA TCCTGTCCGG AGGCTGCTAC   4620

GGTTATGCCG CGAAGCACAT GCACTGGCCG GAGGAGCTGA TTGTGGGCGG ACGGAAGAGG   4680

AACCGCAGCG GACACTTGAG GAAGGCCCAG GCCCTGCAGT CGGTGGTGCA GCTGATGACC   4740

GAGAAGGAAA TGTACGACCA GTGGCAGGAC AACTACAAGG TGCACCATCT TGGATGGACG   4800

CAGGAGAAGG CAGCGGAGGT TTTGAACGCC TGGCAGCGCA ACTTTTCGCG GGAGGTGGAA   4860

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CAGCTGCTAC GTAAACAGTC GAGAATTGCC ACCAACTACG ATATCTACGT GTTCAGCTCG    4920

GCTGCACTGG ATGACATCCT GGCCAAGTTC TCCCATCCCA GCGCCTTGTC CATTGTCATC    4980

GGCGTGGCCG TCACCGTTTT GTATGCCTTT TGCACGCTCC TCCGCTGGAG GGACCCCGTC    5040

CGTGGCCAGA GCAGTGTGGG CGTGGCCGGA GTTCTGCTCA TGTGCTTCAG TACCGCCGCC    5100

GGATTGGGAT TGTCAGCCCT GCTCGGTATC GTTTTCAATG CGCTGACCGC TGCCTATGCG    5160

GAGAGCAATC GGCGGGAGCA GACCAAGCTG ATTCTCAAGA ACGCCAGCAC CCAGGTGGTT    5220

CCGTTTTTGG CCCTTGGTCT GGGCGTCGAT CACATCTTCA TAGTGGGACC GAGCATCCTG    5280

TTCAGTGCCT GCAGCACCGC AGGATCCTTC TTTGCGGCCG CCTTTATTCC GGTGCCGGCT    5340

TTGAAGGTAT TCTGTCTGCA GGCTGCCATC GTAATGTGCT CCAATTTGGC AGCGGCTCTA    5400

TTGGTTTTTC CGGCCATGAT TTCGTTGGAT CTACGGAGAC GTACCGCCGG CAGGGCGGAC    5460

ATCTTCTGCT GCTGTTTTCC GGTGTGGAAG GAACAGCCGA AGGTGGCACC TCCGGTGCTG    5520

CCGCTGAACA ACAACAACGG GCGCGGGGCC CGGCATCCGA AGAGCTGCAA CAACAACAGG    5580

GTGCCGCTGC CCGCCCAGAA TCCTCTGCTG GAACAGAGGG CAGACATCCC TGGGAGCAGT    5640

CACTCACTGG CGTCCTTCTC CCTGGCAACC TTCGCCTTTC AGCACTACAC TCCCTTCCTC    5700

ATGCGCAGCT GGGTGAAGTT CCTGACCGTT ATGGGTTTCC TGGCGGCCCT CATATCCAGC    5760

TTGTATGCCT CCACGCGCCT TCAGGATGGC CTGGACATTA TTGATCTGGT GCCCAAGGAC    5820

AGCAACGAGC ACAAGTTCCT GGATGCTCAA ACTCGGCTCT TTGGCTTCTA CAGCATGTAT    5880

GCGGTTACCC AGGGCAACTT TGAATATCCC ACCCAGCAGC AGTTGCTCAG GGACTACCAT    5940

GATTCCTTTG TGCGGGTGCC ACATGTGATC AAGAATGATA ACGGTGGACT GCCGGACTTC    6000

TGGCTGCTGC TCTTCAGCGA GTGGCTGGGT AATCTGCAAA AAGATATTCG ACGAGGAATA    6060

CCGCGACGGA CGGCTGGACC AAGGAGTGCT GGTTCCCAAA CGCCAGCAGC GATCGCCATC    6120

CTGGCCTACA AGCTAATCGT GCAAACCGGC CATGTGGACA ACCCCGTGGA CAAGGAACTG    6180

GTGCTCACCA ATCGCCTGGT CAACAGCGAT GGCATCATCA ACCAACGCGC CTTCTACAAC    6240

TATCTGTCGG CATGGGCCAC CAACGACGTC TTCGCCTACG GAGCTTCTCA GGTGGGTCTT    6300

CTTATTAAAT TAAATTAAAT TAAATTAAAT TAGATCGCCT TAGTTCTCCT CATATGTACA    6360

TACATATTAT AACTTATCGC ACTCCAAAGT TAAAGATTAC TAAATGTGTG TGTATCTTTA    6420

TTCTTACAGG GCAAATTGTA TCCGGAACCG CGCCAGTATT TTCACCAACC CAACGAGTAC    6480

GATCTTAAGA TACCCAAGAG TCTGCCATTG GTCTACGCTC AGATGCCCTT TTACCTCCAC    6540

GGACTAACAG ATACCTCGCA GATCAAGACC CTGATAGGTC ATATTCGCGA CCTGAGCGTC    6600
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AAGTACGAGG GCTTCGGCCT GCCCAACTAT CCATCGGGTG AGTCGGAAAT GAGTACTTCA    6660

TACATGGGGC CCAACTAACA GTCGATTTAT TTATCGCCAG GCATTCCCTT CATCTTCTGG    6720

GAGCAGTACA TGACCCTGCG CTCCTCACTG GCCATGATCC TGGCCTGCGT GCTACTCGCC    6780

GCCCTGGTGC TGGTCTCCCT GCTCCTGCTC TCCGTTTGGG CCGCCGTTCT CGTGATCCTC    6840

AGCGTTCTGG CCTCGCTGGC CCAGATCTTT GGGGCCATGA CTCTGCTGGG CATCAAACTC    6900

TCGGCCATTC CGGCAGTCAT ACTCATCCTC AGCGTGGGCA TGATGCTGTG CTTCAATGTG    6960

CTGATATCAC TGGTGAGTCT TCATTTCTGG CTGGACCATT AAGAGCTTCG GAGTGAGTCT    7020

TCATTTCTGG CTGGACCATT AAGAGCTTCG GAGTGAGTCT TCATTTCTGG CTGGACCATT    7080

AAGAGCTTCG GATTTTCCAG AGATATCCCA AGACTTTTCA TTGGATCCTC TTCAGCACAC    7140

ATTAATTGCT TATCTTTCCG ATTCTAGGGC TTCATGACAT CCGTTGGCAA CCGACAGCGC    7200

CGCGTCCAGC TGAGCATGCA GATGTCCCTG GGACCACTTG TCCACGGCAT GCTGACCTCC    7260

GGAGTGGCCG TGTTCATGCT CTCCACGTCG CCCTTTGAGT TTGTGATCCG GCACTTCTGC    7320

TGGCTTCTGC TGGTGGTCTT ATGCGTTGGC GCCTGCAACA GCCTTTTGGT GTTCCCCATC    7380

CTACTGAGCA TGGTGGGACC GGAGGCGGAG CTGGTGCCGC TGGAGCATCC AGACCGCATA    7440

TCCACGCCCT CTCCGCTGCC CGTGCGCAGC AGCAAGAGAT CGGGCAAATC CTATGTGGTG    7500

CAGGGATCGC GATCCTCGCG AGGCAGCTGC CAGAAGTCGC ATCACCACCA CCACAAAGAC    7560

CTTAATGATC CATCGCTGAC GACGATCACC GAGGAGCCGC AGTCGTGGAA GTCCAGCAAC    7620

TCGTCCATCC AGATGCCCAA TGATTGGACC TACCAGCCGC GGGAACAGCG ACCCGCCTCC    7680

TACGCGGCCC CGCCCCCCGC CTATCACAAG GCCGCCGCCC AGCAGCACCA CCAGCATCAG    7740

GGCCCGCCCA CAACGCCCCC GCCTCCCTTC CCGACGGCCT ATCCGCCGGA GCTGCAGAGC    7800

ATCGTGGTGC AGCCGGAGGT GACGGTGGAG ACGACGCACT CGGACAGCAA CACCACCAAG    7860

GTGACGGCCA CGGCCAACAT CAAGGTGGAG CTGGCCATCC CGGCAGGCGG TGCGCAGCTA    7920

TAACTTTACG AGTTAGCACT AGCACTAGTT CCTGTAGCTA TTAGGACGTA TCTTTAGACT    7980

CTAGCCTAAG CCGTAACCCT ATTTGTATCT GTAAAATCGA TTTGTCCAGC GGGTCTGCTG    8040

AGGATTTCGT TCTCATGGAT TCTCATGGAT TCTCATGGAT GCTTAAATGG CATGGTAATT    8100

GGCAAAATAT CAATTTTTGT GTCTCAAAAA GATGCATTAG CTTATGGTTT CAAGATACAT    8160

TTTTAAAGAG TCCGCCAGAT ATTTATATAA AAAAAATCCA AAATCGACGT ATCCATGAAA    8220

ATTGAAAAGC TAAGCAGACC CGTATGTATG TATATGTGTA TGCATGTTAG TTAATTTCCC    8280

GAAGTCCGGT ATTTATAGCA GCTGCCTTCC GCGCCCCCCT TCCCTTGAAA TGAACACCCT    8340
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TCCAGCCACG CCCCACCGCC CCTCTGCGTA GCAGCTTTGT ATGTATGTAG TATGCTAGCA        8400

CCTAAGGAAT ACTTAAACTT AGAGATATTT ATTGTAACAC ACGCAAAACA CACACAATGT        8460

ACTTACATAT AATTCAATGC GAGATTCACC CACACAAAAA GGAAACACAA CAAACTAGTA        8520

ATTGTAGCTC GTAATTTAGT TTAAATATGT TACATAAAC ACAAGGACTT GAACCAAAAT         8580

AGTATCGCTT AAACGGAAAC GAGAGAAACG AGAAAAAATA ACTATTACTT AATCAACTAC        8640

AAGAGAGATA TCCCTCCTCC CCTAACCGTA CTTACAACCA AAATAAAACA AGAGTATAAG        8700

CATAAAAATG GAAAACGAAG CGAGGAACGA TTGTAAACGC GGTCATTTAT CCTGTACATT        8760

TGTTGCCCGA AGACTGACTG TCTTTTTTTT AATAAAAATA TATATTATAC AGTTTTTTAA        8820

AAGCGAAATT CATGACTTTT TTTTAACAGT GAGCAGAGAA CAAAAGAAAC GGAAGTTTTC        8880

GCTGTATCAA TAAAAAGATT CCATTTTTTT AATAAATTGT AAAAATCCTA AAAAAAAGAA        8940

GACTACAAAA GTTTAAATTT TTATACGTTA TTGATAAACT TTTATACACG AAAATACTTG        9000

TACTTAGCTA TGATCAACTC CTTGGCTTAA GTCTCGGGTA AG                          9042
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(2) INFORMATION FOR SEQ ID NO:13:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 11 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

    Ile Ile Thr Pro Leu Asp Cys Phe Trp Glu Gly
    1   5   10

(2) INFORMATION FOR SEQ ID NO:14:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 5 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

    Leu Ile Val Gly Gly
    1   5

(2) INFORMATION FOR SEQ ID NO:15:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 7 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

 Pro Phe Phe Trp Glu Gln Tyr
 1   5

(2) INFORMATION FOR SEQ ID NO:16:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 22 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGACGAATTC AAGTCACATT GG   22

(2) INFORMATION FOR SEQ ID NO:17:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 22 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGACGAATTC CTCCCAAACA TC   22

(2) INFORMATION FOR SEQ ID NO:18:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 22 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGACGAATTC TGATGTTTGG GA   22

(2) INFORMATION FOR SEQ ID NO:19:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 22 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGACGAATTC TGATGTTTGG GA   22

(2) INFORMATION FOR SEQ ID NO:20:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 29 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CATACCAGCC AAGCTTGTCG GCCATGCAT   29